

SEQUENCE LISTING

<110> REGENTS OF THE UNIVERSITY OF CALIFORNIA

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ZHANG, Jin

<120> EMISSION RATIO METRIC INDICATORS OF PHOSPHORYLATION

<130> REGEN1550

<160> 42

<170> PatentIn version 3.0

<210> 1

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Glu Leu Asp Gly Asp Val Asn Gly His Lys Phe Ser Val Gly Glu
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Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr Leu Lys Phe Ile Cys
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Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr Leu Val Thr Thr Phe
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Ser Tyr Gly Val Gln Cys Phe Ser Arg Tyr Pro Asp His Met Lys Gln
65 70 75 80cat gac ttt ttc aag agt gcc atg ccc gaa ggt tat gta cag gaa aga
His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly Tyr Val Gln Glu Arg
85 90 95act ata ttt ttc aaa gat gac ggg aac tac aag aca cgt gct gaa gtc
Thr Ile Phe Phe Lys Asp Asp Gly Asn Tyr Lys Thr Arg Ala Glu Val
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Lys Phe Glu Gly Asp Thr Leu Val Asn Arg Ile Glu Leu Lys Gly Ile
115 120 125gat ttt aaa gaa gat gga aac att ctt gga cac aaa ttg gaa tac aac
Asp Phe Lys Glu Asp Gly Asn Ile Leu Gly His Lys Leu Glu Tyr Asn
130 135 140

tat aac tca cac aat gta tac atc atg gca gac aaa caa aag aat gga	480
Tyr Asn Ser His Asn Val Tyr Ile Met Ala Asp Lys Gln Lys Asn Gly	
145 150 155 160	
atc aaa gtt aac ttc aaa att aga cac aac att gaa gat gga agc gtt	528
Ile Lys Val Asn Phe Lys Ile Arg His Asn Ile Glu Asp Gly Ser Val	
165 170 175	
caa cta gca gac cat tat caa caa aat act cca att ggc gat ggc cct	576
Gln Leu Ala Asp His Tyr Gln Gln Asn Thr Pro Ile Gly Asp Gly Pro	
180 185 190	
gtc ctt tta cca gac aac cat tac ctg tcc aca caa tct gcc ctt tcg	624
Val Leu Leu Pro Asp Asn His Tyr Leu Ser Thr Gln Ser Ala Leu Ser	
195 200 205	
aaa gat ccc aac gaa aag aga gac cac atg gtc ctt ctt gag ttt gta	672
Lys Asp Pro Asn Glu Lys Arg Asp His Met Val Ile Leu Glu Phe Val	
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Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr Leu Val Thr Thr Phe	
50 55 60	
Ser Tyr Gly Val Gln Cys Phe Ser Arg Tyr Pro Asp His Met Lys Gln	
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His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly Tyr Val Gln Glu Arg	
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Lys Phe Glu Gly Asp Thr Leu Val Asn Arg Ile Glu Leu Lys Gly Ile	

115

120

125

Asp Phe Lys Glu Asp Gly Asn Ile Leu Gly His Lys Leu Glu Tyr Asn
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Tyr Asn Ser His Asn Val Tyr Ile Met Ala Asp Lys Gln Lys Asn Gly
 145 150 155 160

Ile Lys Val Asn Phe Lys Ile Arg His Asn Ile Glu Asp Gly Ser Val
 165 170 175

Gln Leu Ala Asp His Tyr Gln Gln Asn Thr Pro Ile Gly Asp Gly Pro
 180 185 190

Val Leu Leu Pro Asp Asn His Tyr Leu Ser Thr Gln Ser Ala Leu Ser
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Lys Asp Pro Asn Glu Lys Arg Asp His Met Val Leu Leu Glu Phe Val
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 Val Glu Leu Asp Gly Asp Val Asn Gly His Lys Phe Ser Val Ser Gly
 20 25 30

gag ggc gag ggc gat gcc acc tac ggc aag ctg acc ctg aag ttc atc
 Glu Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr Leu Lys Phe Ile
 35 40 45

tgc acc acc ggc aag ctg ccc gtg ccc tgg ccc acc ctc gtg acc acc
 Cys Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr Leu Val Thr Thr
 50 55 60

ctg acc tac ggc gtg cag tgc ttc agc cgc tac ccc gac cac atg aag
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48

96

144

192

240

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cgc acc atc ttc ttc aag gac gac ggc aac tac aag acc cgc gcc gag	336
Arg Thr Ile Phe Phe Lys Asp Asp Gly Asn Tyr Lys Thr Arg Ala Glu	
100 105 110	
gtg aag ttc gag ggc gac acc ctg gtg aac cgc atc gag ctg aag ggc	384
Val Lys Phe Glu Gly Asp Thr Leu Val Asn Arg Ile Glu Leu Lys Gly	
115 120 125	
atc gac ttc aag gag gac ggc aac atc ctg ggg cac aag ctg gag tac	432
Ile Asp Phe Lys Glu Asp Gly Asn Ile Leu Gly His Lys Leu Glu Tyr	
130 135 140	
aac tac aac agc cac aac gtc tat atc atg gcc gac aag cag aag aac	480
Asn Tyr Asn Ser His Asn Val Tyr Ile Met Ala Asp Lys Gln Lys Asn	
145 150 155 160	
ggc atc aag gtg aac ttc aag atc cgc cac aac atc gag gac ggc agc	528
Gly Ile Lys Val Asn Phe Lys Ile Arg His Asn Ile Glu Asp Gly Ser	
165 170 175	
gtg cag ctc gcc gac cac tac cag cag aac acc ccc atc ggc gac ggc	576
Val Gln Leu Ala Asp His Tyr Gln Gln Asn Thr Pro Ile Gly Asp Gly	
180 185 190	
ccc gtg ctg ctg ccc gac aac cac tac ctg agc acc cag tcc gcc ctg	624
Pro Val Leu Leu Pro Asp Asn His Tyr Leu Ser Thr Gln Ser Ala Leu	
195 200 205	
agc aaa gac ccc aac gag aag cgc gat cac atg gtc ctg ctg gag ttc	672
Ser Lys Asp Pro Asn Glu Lys Arg Asp His Met Val Leu Leu Glu Phe	
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225 230 235	

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Glu Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr Leu Lys Phe Ile
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Cys Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr Leu Val Thr Thr

PDB ID: 1A00

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Arg Thr Ile Phe Phe Lys Asp Asp Gly Asn Tyr Lys Thr Arg Ala Glu
 100 105 110

Val Lys Phe Glu Gly Asp Thr Leu Val Asn Arg Ile Glu Leu Lys Gly
 115 120 125

Ile Asp Phe Lys Glu Asp Gly Asn Ile Leu Gly His Lys Leu Glu Tyr
 130 135 140

Asn Tyr Asn Ser His Asn Val Tyr Ile Met Ala Asp Lys Gln Lys Asn
 145 150 155 160

Gly Ile Lys Val Asn Phe Lys Ile Arg His Asn Ile Glu Asp Gly Ser
 165 170 175

Val Gln Leu Ala Asp His Tyr Gln Gln Asn Thr Pro Ile Gly Asp Gly
 180 185 190

Pro Val Leu Leu Pro Asp Asn His Tyr Leu Ser Thr Gln Ser Ala Leu
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Ser Lys Asp Pro Asn Glu Lys Arg Asp His Met Val Leu Leu Glu Phe
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gag ggc gag ggc gat gcc acc tac ggc aag ctg acc ctg aag ttc atc	144
Glu Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr Leu Lys Phe Ile	
35 40 45	
tgc acc acc ggc aag ctg ccc gtg ccc tgg ccc acc ctc gtg acc acc	192
Cys Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr Leu Val Thr Thr	
50 55 60	
ctg acc tgg ggc gtg cag tgc ttc agc cgc tac ccc gac cac atg aag	240
Leu Thr Trp Gly Val Gln Cys Phe Ser Arg Tyr Pro Asp His Met Lys	
65 70 75 80	
cag cac gac ttc ttc aag tcc gcc atg ccc gaa ggc tac gtc cag gag	288
Gln His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly Tyr Val Gln Glu	
85 90 95	
cgt acc atc ttc ttc aag gac gac ggc aac tac aag acc cgc gcc gag	336
Arg Thr Ile Phe Phe Lys Asp Asp Gly Asn Tyr Lys Thr Arg Ala Glu	
100 105 110	
gtg aag ttc gag ggc gac acc ctg gtg aac cgc atc gag ctg aag ggc	384
Val Lys Phe Glu Gly Asp Thr Leu Val Asn Arg Ile Glu Leu Lys Gly	
115 120 125	
atc gac ttc aag gag gac ggc aac atc ctg ggg cac aag ctg gag tac	432
Ile Asp Phe Lys Glu Asp Gly Asn Ile Leu Gly His Lys Leu Glu Tyr	
130 135 140	
aac tac atc agc cac aac gtc tat atc acc gcc gac aag cag aag aac	480
Asn Tyr Ile Ser His Asn Val Tyr Ile Thr Ala Asp Lys Gln Lys Asn	
145 150 155 160	
ggc atc aag gcc cac ttc aag atc cgc cac aac atc gag gac ggc agc	528
Gly Ile Lys Ala His Phe Lys Ile Arg His Asn Ile Glu Asp Gly Ser	
165 170 175	
gtg cag ctc gcc gac cac tac cag cag aac acc ccc atc ggc gac ggc	576
Val Gln Leu Ala Asp His Tyr Gln Gln Asn Thr Pro Ile Gly Asp Gly	
180 185 190	
ccc gtg ctg ccc gac aac cac tac ctg agc acc cag tcc gcc ctg	624
Pro Val Leu Leu Pro Asp Asn His Tyr Leu Ser Thr Gln Ser Ala Leu	
195 200 205	
agc aaa gac ccc aac gag aag cgc gat cac atg gtc ctg ctg gag ttc	672
Ser Lys Asp Pro Asn Glu Lys Arg Asp His Met Val Leu Leu Glu Phe	
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225 230 235	

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Glu Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr Leu Lys Phe Ile
 35 40 45

Cys Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr Leu Val Thr Thr
 50 55 60

Leu Thr Trp Gly Val Gln Cys Phe Ser Arg Tyr Pro Asp His Met Lys
 65 70 75 80

Gln His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly Tyr Val Gln Glu
 85 90 95

Arg Thr Ile Phe Phe Lys Asp Asp Gly Asn Tyr Lys Thr Arg Ala Glu
 100 105 110

Val Lys Phe Glu Gly Asp Thr Leu Val Asn Arg Ile Glu Leu Lys Gly
 115 120 125

Ile Asp Phe Lys Glu Asp Gly Asn Ile Leu Gly His Lys Leu Glu Tyr
 130 135 140

Asn Tyr Ile Ser His Asn Val Tyr Ile Thr Ala Asp Lys Gln Lys Asn
 145 150 155 160

Gly Ile Lys Ala His Phe Lys Ile Arg His Asn Ile Glu Asp Gly Ser
 165 170 175

Val Gln Leu Ala Asp His Tyr Gln Gln Asn Thr Pro Ile Gly Asp Gly
 180 185 190

Pro Val Leu Leu Pro Asp Asn His Tyr Leu Ser Thr Gln Ser Ala Leu
 195 200 205

Ser Lys Asp Pro Asn Glu Lys Arg Asp His Met Val Leu Leu Glu Phe
 210 215 220

Val Thr Ala Ala Gly Ile Thr Leu Gly Met Asp Glu Leu Tyr Lys
 225 230 235

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Pro Val Leu Leu Pro Asp Asn His Tyr Leu Ser Tyr Gln Ser Ala Leu
 195 200 205

agc aaa gac ccc aac gag aag cgc gat cac atg gtc ctg ctg gag ttc
 Ser Lys Asp Pro Asn Glu Lys Arg Asp His Met Val Leu Leu Glu Phe
 210 215 220

672

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Cys Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr Leu Val Thr Thr
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Phe Gly Tyr Gly Val Gln Cys Phe Ala Arg Tyr Pro Asp His Met Lys
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Gln His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly Tyr Val Gln Glu
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Arg Thr Ile Phe Phe Lys Asp Asp Gly Asn Tyr Lys Thr Arg Ala Glu
 100 105 110

Val Lys Phe Glu Gly Asp Thr Leu Val Asn Arg Ile Glu Leu Lys Gly
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Ile Asp Phe Lys Glu Asp Gly Asn Ile Leu Gly His Lys Leu Glu Tyr
 130 135 140

Asn Tyr Asn Ser His Asn Val Tyr Ile Met Ala Asp Lys Gln Lys Asn
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Gly Ile Lys Val Asn Phe Lys Ile Arg His Asn Ile Glu Asp Gly Ser
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Val Gln Leu Ala Asp His Tyr Gln Gln Asn Thr Pro Ile Gly Asp Gly
 180 185 190

Pro Val Leu Leu Pro Asp Asn His Tyr Leu Ser Tyr Gln Ser Ala Leu
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Val Glu Leu Asp Gly Asp Val Asn Gly His Lys Phe Ser Val Ser Gly	
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gag ggc gag ggc gat gcc acc tac ggc aag ctg acc ctg aag ttc atc	144
Glu Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr Leu Lys Phe Ile	
35 40 45	
tgc acc acc ggc aag ctg ccc gtg ccc acc ctc gtg acc acc	192
Cys Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr Leu Val Thr Thr	
50 55 60	
ttc ggc tac ggc ctg aag tgc ttc gcc cgc tac ccc gac cac atg aag	240
Phe Gly Tyr Gly Leu Lys Cys Phe Ala Arg Tyr Pro Asp His Met Lys	
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cag cac gac ttc ttc aag tcc gcc atg ccc gaa ggc tac gtc cag gag	288
Gln His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly Tyr Val Gln Glu	
85 90 95	
cgc acc atc ttc ttc aag gac gac ggc aac tac aag acc cgc gcc gag	336
Arg Thr Ile Phe Phe Lys Asp Asp Gly Asn Tyr Lys Thr Arg Ala Glu	
100 105 110	
gtg aag ttc gag ggc gac acc ctg gtg aac cgc atc gag ctg aag ggc	384
Val Lys Phe Glu Gly Asp Thr Leu Val Asn Arg Ile Glu Leu Lys Gly	
115 120 125	
atc gac ttc aag gag gac ggc aac atc ctg ggg cac aag ctg gag tac	432

Ile Asp Phe Lys Glu Asp Gly Asn Ile Leu Gly His Lys Leu Glu Tyr
 130 135 140
 aac tac aac agc cac aac gtc tat atc atg gcc gac aag cag aag aac 480
 Asn Tyr Asn Ser His Asn Val Tyr Ile Met Ala Asp Lys Gln Lys Asn
 145 150 155 160
 ggc atc aag gtg aac ttc aag atc cgc cac aac atc gag gac ggc agc 528
 Gly Ile Lys Val Asn Phe Lys Ile Arg His Asn Ile Glu Asp Gly Ser
 165 170 175
 gtc cag ctc gcc gac cac tac cag cag aac acc ccc atc ggc gac ggc 576
 Val Gln Leu Ala Asp His Tyr Gln Gln Asn Thr Pro Ile Gly Asp Gly
 180 185 190
 ccc gtg ctg ctg ccc gac aac cac tac ctg agc tac cag tcc gcc ctg 624
 Pro Val Leu Leu Pro Asp Asn His Tyr Leu Ser Tyr Gln Ser Ala Leu
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 Ser Lys Asp Pro Asn Glu Lys Arg Asp His Met Val Leu Leu Glu Phe
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 Phe Gly Tyr Gly Leu Lys Cys Phe Ala Arg Tyr Pro Asp His Met Lys
 65 70 75 80
 Gln His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly Tyr Val Gln Glu
 85 90 95
 Arg Thr Ile Phe Phe Lys Asp Asp Gly Asn Tyr Lys Thr Arg Ala Glu
 100 105 110

Val Lys Phe Glu Gly Asp Thr Leu Val Asn Arg Ile Glu Leu Lys Gly
 115 120 125

Ile Asp Phe Lys Glu Asp Gly Asn Ile Leu Gly His Lys Leu Glu Tyr
 130 135 140

Asn Tyr Asn Ser His Asn Val Tyr Ile Met Ala Asp Lys Gln Lys Asn
 145 150 155 160

Gly Ile Lys Val Asn Phe Lys Ile Arg His Asn Ile Glu Asp Gly Ser
 165 170 175

Val Gln Leu Ala Asp His Tyr Gln Gln Asn Thr Pro Ile Gly Asp Gly
 180 185 190

Pro Val Leu Leu Pro Asp Asn His Tyr Leu Ser Tyr Gln Ser Ala Leu
 195 200 205

Ser Lys Asp Pro Asn Glu Lys Arg Asp His Met Val Leu Leu Glu Phe
 210 215 220

Val Thr Ala Ala Gly Ile Thr Leu Gly Met Asp Glu Leu Tyr Lys
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 Met Glu Gly Thr Val Asn Gly His Glu Phe Glu Ile Glu Gly Glu Gly
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 Glu Gly Arg Pro Tyr Glu Gly His Asn Thr Val Lys Leu Lys Val Thr
 35 40 45

aag ggg gga cct ttg cca ttt gct tgg gat att ttg tca cca caa ttt 248

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150							155					160							
cat	aag	gct	ctg	aag	ctg	aaa	gac	ggt	gat	cat	tac	cta	gtt	gaa	ttc		584		
His	Lys	Ala	Leu	Lys	Leu	Lys	Asp	Gly	Gly	His	Tyr	Leu	Val	Glu	Phe				
165							170					175							
aaa	agt	att	tac	atg	gca	aag	aag	cct	gtg	cag	cta	cca	ggg	tac	tac		632		
Lys	Ser	Ile	Tyr	Met	Ala	Lys	Lys	Pro	Val	Gln	Leu	Pro	Gly	Tyr	Tyr				
180							185					190							
tat	gtt	gac	tcc	aaa	ctg	gat	ata	aca	agc	cac	aac	gaa	gac	tat	aca		680		
Tyr	Val	Asp	Ser	Lys	Leu	Asp	Ile	Thr	Ser	His	Asn	Glu	Asp	Tyr	Thr				
195							200					205							
atc	gtt	gag	cag	tat	gaa	aga	acc	gag	gga	cgc	cac	cat	ctg	ttc	ctt		728		
Ile	Val	Glu	Gln	Tyr	Glu	Arg	Thr	Glu	Gly	Arg	His	His	Leu	Phe	Leu				
210							215				220		225						
taa	ggctgaactt	ggctcagacg	tgggtgagcg	gtaatgacca	caaaaggcag												781		
cgaagaaaaa	ccatgatcgt	tttttttagg	ttggcagcct	gaaatcgtag	gaaatacatac												841		
agaaaatgtt	caaacagg																859		

<210> 12
 <211> 225
 <212> PRT
 <213> Discosoma sp.

<400> 12

Met Arg Ser Ser Lys Asn Val Ile Lys Glu Phe Met Arg Phe Lys Val
 1 5 10 15

Arg Met Glu Gly Thr Val Asn Gly His Glu Phe Glu Ile Glu Gly Glu
 20 25 30

Gly Glu Gly Arg Pro Tyr Glu Gly His Asn Thr Val Lys Leu Lys Val
 35 40 45

Thr Lys Gly Gly Pro Leu Pro Phe Ala Trp Asp Ile Leu Ser Pro Gln
 50 55 60

Phe Gln Tyr Gly Ser Lys Val Tyr Val Lys His Pro Ala Asp Ile Pro
 65 70 75 80

Asp Tyr Lys Lys Leu Ser Phe Pro Glu Gly Phe Lys Trp Glu Arg Val
 85 90 95

Met Asn Phe Glu Asp Gly Gly Val Val Thr Val Thr Gln Asp Ser Ser
 100 105 110

Leu Gln Asp Gly Cys Phe Ile Tyr Lys Val Lys Phe Ile Gly Val Asn
 115 120 125

Phe Pro Ser Asp Gly Pro Val Met Gln Lys Lys Thr Met Gly Trp Glu
 130 135 140

Ala Ser Thr Glu Arg Leu Tyr Pro Arg Asp Gly Val Leu Lys Gly Glu
 145 150 155 160

Ile His Lys Ala Leu Lys Leu Lys Asp Gly Gly His Tyr Leu Val Glu
 165 170 175

Phe Lys Ser Ile Tyr Met Ala Lys Lys Pro Val Gln Leu Pro Gly Tyr
 180 185 190

Tyr Tyr Val Asp Ser Lys Leu Asp Ile Thr Ser His Asn Glu Asp Tyr
 195 200 205

Thr Ile Val Glu Gln Tyr Glu Arg Thr Glu Gly Arg His His Leu Phe
 210 215 220

Leu
 225

<210> 13
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<220>
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Gly Ser Thr Ser Gly Ser Gly Lys Pro Gly Ser Gly Glu Gly Ser Thr
1 5 10 15
Lys Gly

<210> 14
<211> 8
<212> PRT
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<220>
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<220>
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<223> Phosphorylated peptide

<400> 14
Asp Tyr Ile Ile Pro Leu Pro Asp
1 5

<210> 15
<211> 9
<212> PRT
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<220>
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<220>
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<400> 15
His Ile Ile Glu Asn Pro Gln Tyr Phe
1 5

<210> 16
<211> 8
<212> PRT
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<220>
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<220>
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Ala Arg Ser His Ser Tyr Pro Ala
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<211> 6
<212> PRT
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<222> (3)..(4)
<223> Xaa is any Amino Acid
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<400> 17

Cys Cys Xaa Xaa Cys Cys
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<210> 18
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<213> Artificial sequence

<220>
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<400> 18

Cys Arg Gln Ile Lys Trp Phe Asn Arg Arg Met Lys Trp Lys Lys
1 5 10 15

<210> 19
<211> 7
<212> PRT
<213> Artificial sequence

<220>
<223> Synthetic peptide

<400> 19

Ala Gly Gly Thr Gly Gly Ser
1 5

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<210> 20
<211> 7
<212> PRT
<213> Artificial sequence
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<220>
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<400> 20

Leu Arg Arg Ala Ser Leu Pro
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<210> 21
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<400> 21

Gly Gly Thr Gly Gly Ser Glu Leu
1 5

<210> 22
<211> 9
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<400> 22

Gly Ser His Ser Gly Ser Gly Lys Pro
1 5

<210> 23
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<400> 23

Glu Glu Glu Ala Glu Tyr Met Asn Met Ala Pro Gln Ser
1 5 10

<210> 24
<211> 15
<212> PRT
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<400> 24

Gly Ser Thr Ser Gly Ser Gly Lys Pro Gly Ser Gly Glu Gly Ser
1 5 10 15

<210> 25
<211> 6
<212> PRT
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<220>
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<400> 25

Glu Ile Tyr Gly Glu Phe
1 5

<210> 26

<211> 34

<212> DNA

<213> Artificial sequence

<220>

<223> Forward primer for PCR

<400> 26

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34

<210> 27

<211> 92

<212> DNA

<213> Artificial sequence

<220>

<223> Reverse primer for PCR

<400> 27

cgcggagctc gctgccgccc gtgccgccc ggctggcgcg acggaggctg ccggccgggtgc

60

cgcctgcaga gtctgatgtc caaagtgtta gg

92

<210> 28

<211> 33

<212> DNA

<213> Artificial sequence

<220>

<223> Primer for PCR

<400> 28

cgtcgcccca gcctgccagg caccggcgcc agc

33

<210> 29

<211> 33

<212> DNA

<213> Artificial sequence

<220>

<223> Primer for PCR

<400> 29

gctgccgccc gtggctggca ggctggcgcg acg

33

<210> 30

<211> 32

<212> DNA

<213> Artificial sequence

<220>

<223> Primer for PCR

<400> 30

gcctccgtcg cgccgcactg ccaggcacccg gc

32

<210> 31

<211> 32

<212> DNA

<213> Artificial sequence

<220>

<223> Primer for PCR

<400> 31

gccgggtgcct ggcagtgcgg cgcgacggag gc

32

<210> 32

<211> 7

<212> PRT

<213> Artificial sequence

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<223> Synthetic peptide

<400> 32

Leu Arg Arg Ala Ser Leu Gly

1 5

<210> 33

<211> 9

<212> PRT

<213> Artificial sequence

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<223> Synthetic peptide

<400> 33

Ala Gln Arg Ser Thr Ser Thr Pro Asn

1 5

<210> 34

<211> 6

<212> PRT

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<223> Synthetic peptide

<220>

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<223> Xaa is any Amino Acid

<400> 34

Arg Ser Xaa Ser Xaa Pro
1 5

<210> 35
<211> 4
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<220>
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<222> (3)..(3)
<223> Xaa is any Amino Acid

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Arg Arg Xaa Ser
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<210> 36
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<220>
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<223> Xaa is Serine or Threonine

<400> 36

Arg Xaa Xaa Xaa
1

<210> 37
<211> 4
<212> PRT
<213> Artificial sequence

<220>
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<220>
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<223> Xaa is Lysine or Arginine

<220>
 <221> VARIANT
 <222> (2)..(3)
 <223> Xaa is any Amino Acid

<220>
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 <223> Xaa is Serine or Threonine

<400> 37

Xaa Xaa Xaa Xaa
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<210> 38
 <211> 39
 <212> DNA
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<220>
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<400> 38
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39

<210> 39
 <211> 99
 <212> DNA
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<220>
 <223> Reverse primer for PCR

<400> 39
 taccatgagc tctgattgcg gagccatgtt catgtactca gtttcctttt caggcttccc

60

agatccagag tgagacccca cgggttgctc taggcacag

99

<210> 40
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 <212> DNA
 <213> Artificial sequence

<220>
 <223> Forward primer for PCR

<400> 40
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35

<210> 41
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tccagatgt a gacccacaga cgtagtcag gcg 93

<210> 42
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<220>
<223> Synthetic peptide

<220>
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<222> (2)..(2)
<223> Xaa is Arginine or Lysine

<220>
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<222> (3)..(3)
<223> Xaa is Phenylalanine, Arginine, Serine or Asparagine

<220>
<221> VARIANT
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<223> Xaa is Arginine, Histidine, Lysine

<220>
<221> VARIANT
<222> (5)..(5)
<223> Phosphorylated peptide

<220>
<221> VARIANT
<222> (6)..(6)
<223> Xaa is Tryptophan, Tyrosine, Phenylalanine, Leucine

<400> 42

Arg Xaa Xaa Xaa Ser Xaa Pro
1 5